

12-10-01

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schulein, Martin  
Andersen, Lene N.  
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(ii) TITLE OF INVENTION: Novel Endoglucanases

(iii) NUMBER OF SEQUENCES: 109

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novo Nordisk of North America, Inc.  
(B) STREET: 405 Lexington Avenue, 64th Floor  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: United States of America  
(F) ZIP: 10174-6401

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 10/007,521  
(B) FILING DATE: 10 December 2001  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lambiris, Elias J.  
(B) REGISTRATION NUMBER: 33,728  
(C) REFERENCE/DOCKET NUMBER: 4366.200-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-867-0123  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 960 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 113..787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAGAAAGGC TCTCTGCTGT CGTCGCTCTC GTCGCTCTCG TCGGCATCCT CCATCCGTCC	60
GCCTTTGATA ACCCGCTCCC CGACTCAGTC AAGACGACGC ATACTTGGCA CC ATG	115
Met	
1	
CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC CTG	163
His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala Leu	
5 10 15	
GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC TGC	211
Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys Cys	
20 25 30	
AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG CAG	259
Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val Gln	
35 40 45	
GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC CGG	307
Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr Arg	
50 55 60 65	
TCC GGC TGC GAC GCG GGC GGC AGC GCC TAC ATG TGC TCC TCC CAG AGC	355
Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln Ser	
70 75 80	
CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC AAG	403
Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val Lys	
85 90 95	
CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG CTG	451
Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu Leu	
100 105 110	
ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG GCG	499
Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln Ala	
115 120 125	
ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC ATC	547
Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala Ile	
130 135 140 145	
CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC GGC	595
Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr Gly	
150 155 160	
GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC AAG	643
Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser Lys	
165 170 175	

GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC TGG	691
Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn Trp	
180 185 190	
CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC CAG	739
Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe Gln	
195 200 205	
GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC CGT	787
Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser Arg	
210 215 220 225	
TAAGAGGGAA GAGAGGGGGC TGGAAGGACC GAAAGATTCA ACCTCTGCTC CTGCTGGGGA	847
AGCTCGGGCG CGAGTGTGAA ACTGGTGTAAT ATATTGTGGC ACACACAAGC TACTACAGTC	907
CGTCTCGCCG TCCGGCTAAC TAGCCTTGCT GCGGATCTGT CCAAAAAAAAA AAA	960

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala	
1 5 10 15	
Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys	
20 25 30	
Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val	
35 40 45	
Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr	
50 55 60	
Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln	
65 70 75 80	
Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val	
85 90 95	
Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu	
100 105 110	
Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln	
115 120 125	
Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala	
130 135 140	

Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr  
145 150 155 160

Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser  
165 170 175

Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn  
180 185 190

Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe  
195 200 205

Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser  
210 215 220

Arg  
225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC	48
Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala	
230 235 240	
CTG GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC	96
Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys	
245 250 255	
TGC AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG	144
Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val	
260 265 270	
CAG GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC	192
Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr	
275 280 285	
CGG TCC GGC TGC GAC GCG GGC GGC AGC GCC TAC ATG TGC TCC TCC CAG	240
Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln	
290 295 300 305	

AGC CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC	288
Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val	
310 315 320	
AAG CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG	336
Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu	
325 330 335	
CTG ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG	384
Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln	
340 345 350	
GCG ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC	432
Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala	
355 360 365	
ATC CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC	480
Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr	
370 375 380 385	
GGC GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC	528
Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser	
390 395 400	
AAG GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC	576
Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn	
405 410 415	
TGG CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC	624
Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe	
420 425 430	
CAG GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC	672
Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser	
435 440 445	
CGT CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC	720
Arg Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr	
450 455 460 465	
AGC ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG	768
Ser Thr Thr Ser Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr	
470 475 480	
ACT CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT	816
Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn	
485 490 495	
GGC TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG	864
Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys	
500 505 510	
ATT AAT GAC TGG TAC CAT CAG TGC CTG TAG	894
Ile Asn Asp Trp Tyr His Gln Cys Leu	
515 520	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	His	Leu	Ser	Ala	Thr	Thr	Gly	Phe	Leu	Ala	Leu	Pro	Val	Leu	Ala	
1				5					10					15		
Leu	Asp	Gln	Leu	Ser	Gly	Ile	Gly	Gln	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	
		20						25					30			
Cys	Lys	Pro	Ser	Cys	Ala	Trp	Pro	Gly	Lys	Gly	Pro	Ser	Ser	Pro	Val	
		35						40				45				
Gln	Ala	Cys	Asp	Lys	Asn	Asp	Asn	Pro	Leu	Asn	Asp	Gly	Gly	Ser	Thr	
	50					55					60					
Arg	Ser	Gly	Cys	Asp	Ala	Gly	Gly	Ser	Ala	Tyr	Met	Cys	Ser	Ser	Gln	
65					70					75					80	
Ser	Pro	Trp	Ala	Val	Ser	Asp	Glu	Leu	Ser	Tyr	Gly	Trp	Ala	Ala	Val	
				85					90					95		
Lys	Leu	Ala	Gly	Ser	Ser	Glu	Ser	Gln	Trp	Cys	Cys	Ala	Cys	Tyr	Glu	
		100						105					110			
Leu	Thr	Phe	Thr	Ser	Gly	Pro	Val	Ala	Gly	Lys	Lys	Met	Ile	Val	Gln	
	115						120					125				
Ala	Thr	Asn	Thr	Gly	Gly	Asp	Leu	Gly	Asp	Asn	His	Phe	Asp	Leu	Ala	
	130					135					140					
Ile	Pro	Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Ala	Cys	Thr	Asp	Gln	Tyr	
145					150					155					160	
Gly	Ala	Pro	Pro	Asn	Gly	Trp	Gly	Asp	Arg	Tyr	Gly	Gly	Ile	His	Ser	
				165					170					175		
Lys	Glu	Glu	Cys	Glu	Ser	Phe	Pro	Glu	Ala	Leu	Lys	Pro	Gly	Cys	Asn	
		180						185					190			
Trp	Arg	Phe	Asp	Trp	Phe	Gln	Asn	Ala	Asp	Asn	Pro	Ser	Val	Thr	Phe	
		195					200					205				
Gln	Glu	Val	Ala	Cys	Pro	Ser	Glu	Leu	Thr	Ser	Lys	Ser	Gly	Cys	Ser	
	210					215					220					
Arg	Pro	Ser	Ser	Ser	Thr	Ser	Ser	Pro	Val	Asn	Gln	Pro	Thr	Ser	Thr	
225					230					235					240	

Ser Thr Thr Ser Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr  
 245 250 255

Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn  
 260 265 270

Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys  
 275 280 285

Ile Asn Asp Trp Tyr His Gln Cys Leu  
 290 295

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 927 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC	48
Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala	
300 305 310	
CTG GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC	96
Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys	
315 320 325	
TGC AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG	144
Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val	
330 335 340 345	
CAG GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC	192
Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr	
350 355 360	
CGG TCC GGC TGC GAC GCG GGC GGC AGC GCC TAC ATG TGC TCC TCC CAG	240
Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln	
365 370 375	
AGC CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC	288
Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val	
380 385 390	
AAG CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG	336
Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu	
395 400 405	

CTG ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG	384
Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln	
410 415 420 425	
GCG ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC	432
Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala	
430 435 440	
ATC CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC	480
Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr	
445 450 455	
GGC GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC	528
Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser	
460 465 470	
AAG GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC	576
Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn	
475 480 485	
TGG CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC	624
Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe	
490 495 500 505	
CAG GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC	672
Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser	
510 515 520	
CGT AAC GAC GAC GGC AAC TTC CCT GCC GTC CAG ATC CCC TCC AGC AGC	720
Arg Asn Asp Asp Gly Asn Phe Pro Ala Val Gln Ile Pro Ser Ser Ser	
525 530 535	
ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC AGC ACC ACG TCC ACC	768
Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr Ser Thr	
540 545 550	
TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG ACT CCC AGC GGC TGC	816
Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly Cys	
555 560 565	
ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT GGC TGG AGC GGC TGC	864
Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys	
570 575 580 585	
ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG ATT AAT GAC TGG TAC	912
Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr	
590 595 600	
CAT CAG TGC CTG TAG	927
His Gln Cys Leu	
605	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids



(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Leu	Ser	Ala	Thr	Thr	Gly	Phe	Leu	Ala	Leu	Pro	Val	Leu	Ala
1				5					10					15	
Leu	Asp	Gln	Leu	Ser	Gly	Ile	Gly	Gln	Thr	Thr	Arg	Tyr	Trp	Asp	Cys
		20						25					30		
Cys	Lys	Pro	Ser	Cys	Ala	Trp	Pro	Gly	Lys	Gly	Pro	Ser	Ser	Pro	Val
		35					40					45			
Gln	Ala	Cys	Asp	Lys	Asn	Asp	Asn	Pro	Leu	Asn	Asp	Gly	Gly	Ser	Thr
	50					55					60				
Arg	Ser	Gly	Cys	Asp	Ala	Gly	Gly	Ser	Ala	Tyr	Met	Cys	Ser	Ser	Gln
65					70					75					80
Ser	Pro	Trp	Ala	Val	Ser	Asp	Glu	Leu	Ser	Tyr	Gly	Trp	Ala	Ala	Val
				85					90						95
Lys	Leu	Ala	Gly	Ser	Ser	Glu	Ser	Gln	Trp	Cys	Cys	Ala	Cys	Tyr	Glu
			100					105					110		
Leu	Thr	Phe	Thr	Ser	Gly	Pro	Val	Ala	Gly	Lys	Lys	Met	Ile	Val	Gln
		115					120					125			
Ala	Thr	Asn	Thr	Gly	Gly	Asp	Leu	Gly	Asp	Asn	His	Phe	Asp	Leu	Ala
		130				135					140				
Ile	Pro	Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Ala	Cys	Thr	Asp	Gln	Tyr
145					150				155						160
Gly	Ala	Pro	Pro	Asn	Gly	Trp	Gly	Asp	Arg	Tyr	Gly	Gly	Ile	His	Ser
				165				170						175	
Lys	Glu	Glu	Cys	Glu	Ser	Phe	Pro	Glu	Ala	Leu	Lys	Pro	Gly	Cys	Asn
			180					185					190		
Trp	Arg	Phe	Asp	Trp	Phe	Gln	Asn	Ala	Asp	Asn	Pro	Ser	Val	Thr	Phe
		195					200					205			
Gln	Glu	Val	Ala	Cys	Pro	Ser	Glu	Leu	Thr	Ser	Lys	Ser	Gly	Cys	Ser
		210					215				220				
Arg	Asn	Asp	Asp	Gly	Asn	Phe	Pro	Ala	Val	Gln	Ile	Pro	Ser	Ser	Ser
225					230					235					240
Thr	Ser	Ser	Pro	Val	Asn	Gln	Pro	Thr	Ser	Thr	Ser	Thr	Thr	Ser	Thr
				245					250					255	
Ser	Thr	Thr	Ser	Ser	Pro	Pro	Val	Gln	Pro	Thr	Thr	Pro	Ser	Gly	Cys
				260				265					270		

Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys  
 275 280 285

Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr  
 290 295 300

His Gln Cys Leu  
 305

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 51..935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAGTGTGCT GGAAAGCCTT CGTGCTGTCC CCGACGTATC CCTGACCGCC ATG CGT	56
Met Arg	
310	
TCC ACC AGC ATC TTG ATC GGC CTT GTT GCC GGC GTC GCT GCT CAG AGC	104
Ser Thr Ser Ile Leu Ile Gly Leu Val Ala Gly Val Ala Ala Gln Ser	
315 320 325	
TCT GGC TCT GGC CAT ACA ACC AGG TAC TGG GAC TGC TGC AAG CCC TCA	152
Ser Gly Ser Gly His Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser	
330 335 340	
TGC GCC TGG GAT GAG AAG GCG GCT GTC AGC CGG CCG GTC ACA ACA TGC	200
Cys Ala Trp Asp Glu Lys Ala Ala Val Ser Arg Pro Val Thr Thr Cys	
345 350 355	
GAC AGG AAC AAC AGC CCC CTT TCG CCC GGC GCT GTG AGC GGC TGC GAC	248
Asp Arg Asn Asn Ser Pro Leu Ser Pro Gly Ala Val Ser Gly Cys Asp	
360 365 370	
CCC AAC GGC GTT GCA TTC ACC TGC AAC GAC AAC CAG CCT TGG GCC GTA	296
Pro Asn Gly Val Ala Phe Thr Cys Asn Asp Asn Gln Pro Trp Ala Val	
375 380 385 390	
AAC AAC AAT GTC GCC TAC GGT TTT GCG GCT ACC GCC TTC CCT GGT GGC	344
Asn Asn Asn Val Ala Tyr Gly Phe Ala Ala Thr Ala Phe Pro Gly Gly	
395 400 405	

AAT GAG GCG TCG TGG TGC TGT GCC TGC TAT GCT CTT CAA TTC ACA TCC	392
Asn Glu Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe Thr Ser	
410 415 420	
GGC CCC GTT GCT GGC AAG ACG ATG GTT GTG CAA TCC ACC AAC ACT GGC	440
Gly Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn Thr Gly	
425 430 435	
GGA GAT CTC AGC GGC ACT CAC TTC GAT ATC CAG ATG CCC GGT GGA GGT	488
Gly Asp Leu Ser Gly Thr His Phe Asp Ile Gln Met Pro Gly Gly Gly	
440 445 450	
CTC GGC ATC TTC GAC GGC TGC ACC CCG CAG TTC GGC TTC ACG TTC CCC	536
Leu Gly Ile Phe Asp Gly Cys Thr Pro Gln Phe Gly Phe Thr Phe Pro	
455 460 465 470	
GGC AAC CGC TAC GGC GGT ACC ACG AGC CGC AGC CAG TGC GCC GAG CTG	584
Gly Asn Arg Tyr Gly Gly Thr Thr Ser Arg Ser Gln Cys Ala Glu Leu	
475 480 485	
CCC TCC GTC CTC CGT GAC GGC TGC CAC TGG CGT TAC GAC TGG TTC AAC	632
Pro Ser Val Leu Arg Asp Gly Cys His Trp Arg Tyr Asp Trp Phe Asn	
490 495 500	
GAT GCC GAC AAC CCC AAC GTC AAC TGG CGC CGC GTC CGA TGC CCG GCG	680
Asp Ala Asp Asn Pro Asn Val Asn Trp Arg Arg Val Arg Cys Pro Ala	
505 510 515	
GCC CTC ACG AAC CGC TCC GGC TGC GTC CGC AAC GAC GAC AAC AGC TAC	728
Ala Leu Thr Asn Arg Ser Gly Cys Val Arg Asn Asp Asp Asn Ser Tyr	
520 525 530	
CCC GTC TTC GAG CCC GGC ACG GGC ACC CCG CCG ACC CCC ACG ACC ACG	776
Pro Val Phe Glu Pro Gly Thr Gly Thr Pro Pro Thr Pro Thr Thr Thr	
535 540 545 550	
ACT ACC AGC TCC CCT CCT CAG CCC ACC AAC GGC GGA GGC GGC GGC ACT	824
Thr Thr Ser Ser Pro Pro Gln Pro Thr Asn Gly Gly Gly Gly Gly Thr	
555 560 565	
TCT CCT CAC TGG GGC CAG TGC GGC GGC CAG GGC TGG TCT GGC CCG ACG	872
Ser Pro His Trp Gly Gln Cys Gly Gln Gly Trp Ser Gly Pro Thr	
570 575 580	
GCC TGT GCC GGT GGG TCG ACC TGC AAC CTG ATC AAC CCG TGG TAC TCC	920
Ala Cys Ala Gly Gly Ser Thr Cys Asn Leu Ile Asn Pro Trp Tyr Ser	
585 590 595	
CAG TGC ATT CCC AAC TAAGTGATCC GGGCATTGCG GTCGAAAGGG GACCGT TAGT	975
Gln Cys Ile Pro Asn	
600	
CGACAAGGCC CAGCCAGACC TCAGGCAGGT GGCTGCCATG GCAGATTGTA TATAGTCTTC	1035
CGAGTACATA CTATTGAATG AAAATAAGAG CGGCTCGGAC CATGAGCAGA TGCCATTGTA	1095
TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1154

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Ser Thr Ser Ile Leu Ile Gly Leu Val Ala Gly Val Ala Ala  
1 5 10 15  
Gln Ser Ser Gly Ser Gly His Thr Thr Arg Tyr Trp Asp Cys Cys Lys  
20 25 30  
Pro Ser Cys Ala Trp Asp Glu Lys Ala Ala Val Ser Arg Pro Val Thr  
35 40 45  
Thr Cys Asp Arg Asn Asn Ser Pro Leu Ser Pro Gly Ala Val Ser Gly  
50 55 60  
Cys Asp Pro Asn Gly Val Ala Phe Thr Cys Asn Asp Asn Gln Pro Trp  
65 70 75 80  
Ala Val Asn Asn Asn Val Ala Tyr Gly Phe Ala Ala Thr Ala Phe Pro  
85 90 95  
Gly Gly Asn Glu Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe  
100 105 110  
Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn  
115 120 125  
Thr Gly Gly Asp Leu Ser Gly Thr His Phe Asp Ile Gln Met Pro Gly  
130 135 140  
Gly Gly Leu Gly Ile Phe Asp Gly Cys Thr Pro Gln Phe Gly Phe Thr  
145 150 155 160  
Phe Pro Gly Asn Arg Tyr Gly Gly Thr Thr Ser Arg Ser Gln Cys Ala  
165 170 175  
Glu Leu Pro Ser Val Leu Arg Asp Gly Cys His Trp Arg Tyr Asp Trp  
180 185 190  
Phe Asn Asp Ala Asp Asn Pro Asn Val Asn Trp Arg Arg Val Arg Cys  
195 200 205  
Pro Ala Ala Leu Thr Asn Arg Ser Gly Cys Val Arg Asn Asp Asp Asn  
210 215 220  
Ser Tyr Pro Val Phe Glu Pro Gly Thr Gly Thr Pro Pro Thr Pro Thr  
225 230 235 240

Thr Thr Thr Thr Ser Ser Pro Pro Gln Pro Thr Asn Gly Gly Gly Gly  
 245 250 255

Gly Thr Ser Pro His Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly  
 260 265 270

Pro Thr Ala Cys Ala Gly Gly Ser Thr Cys Asn Leu Ile Asn Pro Trp  
 275 280 285

Tyr Ser Gln Cys Ile Pro Asn  
 290 295

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 110..1156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAGTTCTGG CCGGAACAGA TCTCCGTTGT CGATCTTCGA TTTTCCAGAC TCAGTCTGTG	60
ACACTCCTTC AATCCACATT CCTTTACTTC TTCGTCCTC ATTCACATC ATG ATT	115
	Met Ile
TCA GCT TGG ATT CTC CTG GGG CTG GTA GGC GCC GTG CCC TCC TCC GTC	163
Ser Ala Trp Ile Leu Leu Gly Leu Val Gly Ala Val Pro Ser Ser Val	
300 305 310	
ATG GCC GCC TCG GGC AAA GGC CAC ACC ACC CGC TAC TGG GAT TGC TGC	211
Met Ala Ala Ser Gly Lys Gly His Thr Thr Arg Tyr Trp Asp Cys Cys	
315 320 325	
AAG ACT TCT TGC GCA TGG GAG GGC AAG GCA TCC GTC TCC GAG CCT GTC	259
Lys Thr Ser Cys Ala Trp Glu Gly Lys Ala Ser Val Ser Glu Pro Val	
330 335 340 345	
CTG ACC TGT AAC AAG CAG GAC AAC CCC ATC GTC GAT GCC AAC GCC AGA	307
Leu Thr Cys Asn Lys Gln Asp Asn Pro Ile Val Asp Ala Asn Ala Arg	
350 355 360	
AGC GGC TGC GAC GGC GGC GGG GCA TTT GCC TGT ACC AAC AAT TCC CCT	355
Ser Gly Cys Asp Gly Gly Gly Ala Phe Ala Cys Thr Asn Asn Ser Pro	
365 370 375	

TGG GCC GTG AGC GAG GAC CTG GCC TAC GGA TTT GCT GCC ACA GCC CTC	403
Trp Ala Val Ser Glu Asp Leu Ala Tyr Gly Phe Ala Ala Thr Ala Leu	
380 385 390	
AGC GGC GGC ACT GAG GGC AGC TGG TGC TGC GCG TGT TAC GCC ATC ACA	451
Ser Gly Gly Thr Glu Gly Ser Trp Cys Cys Ala Cys Tyr Ala Ile Thr	
395 400 405	
TTC ACG AGT GGC CCT GTG GCT GGC AAG AAG ATG GTC GTC CAG TCC ACG	499
Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Val Val Gln Ser Thr	
410 415 420 425	
AAC ACG GGA GGC GAC CTG TCC AAC AAC CAC TTT GAC CTG ATG ATT CCC	547
Asn Thr Gly Gly Asp Leu Ser Asn Asn His Phe Asp Leu Met Ile Pro	
430 435 440	
GGT GGA GGC CTC GGC ATC TTT GAC GGT TGC TCG GCT CAG TTC GGA CAA	595
Gly Gly Gly Leu Gly Ile Phe Asp Gly Cys Ser Ala Gln Phe Gly Gln	
445 450 455	
CTT CTT CCC GGC GAG CGT TAC GGA GGT GTT TCG TCC CGC TCT CAA TGC	643
Leu Leu Pro Gly Glu Arg Tyr Gly Gly Val Ser Ser Arg Ser Gln Cys	
460 465 470	
GAT GGC ATG CCC GAG CTC TTG AAA GAC GGT TGC CAG TGG CGC TTC GAC	691
Asp Gly Met Pro Glu Leu Leu Lys Asp Gly Cys Gln Trp Arg Phe Asp	
475 480 485	
TGG TTC AAG AAC TCA GAC AAC CCT GAC ATC GAG TTC GAG CAG GTC CAG	739
Trp Phe Lys Asn Ser Asp Asn Pro Asp Ile Glu Phe Glu Gln Val Gln	
490 495 500 505	
TGT CCC AAA GAG CTC ATT GCG GTC TCT GGG TGC GTC CGT GAC GAC GAT	787
Cys Pro Lys Glu Leu Ile Ala Val Ser Gly Cys Val Arg Asp Asp Asp	
510 515 520	
AGC AGC TTT CCC GTC TTC CAA GGT TCG GGC TCA GGA GAT GTC AAC CCA	835
Ser Ser Phe Pro Val Phe Gln Gly Ser Gly Ser Gly Asp Val Asn Pro	
525 530 535	
CCT CCC AAG CCG ACT ACG ACT ACG ACC TCG TCA AAG CCG AAA ACA ACC	883
Pro Pro Lys Pro Thr Thr Thr Thr Ser Ser Lys Pro Lys Thr Thr	
540 545 550	
TCT GCA CCA TCC ACT CTC TCG AAC CCA TCC GCC CCT CAA CAG CCA GGG	931
Ser Ala Pro Ser Thr Leu Ser Asn Pro Ser Ala Pro Gln Gln Pro Gly	
555 560 565	
AAC ACT GAT AGA CCT GCC GAG ACA ACC ACT ACC AAG CTG CCT GCC CTG	979
Asn Thr Asp Arg Pro Ala Glu Thr Thr Thr Lys Leu Pro Ala Leu	
570 575 580 585	
CCG GCC ACG ACG AGC AGC CCT GCT GTC TCA GTT CCT TCG TCC AGC GCT	1027
Pro Ala Thr Thr Ser Ser Pro Ala Val Ser Val Pro Ser Ser Ala	
590 595 600	

CGC GTG CCT TTG TGG GGG CAA TGC GAC TCG GAA GCT TCA TGG GAC GCA 1075  
 Arg Val Pro Leu Trp Gly Gln Cys Asp Ser Glu Ala Ser Trp Asp Ala  
                   605                                  610                                  615

CCT AAG AAG TGT GCA AAG GGC ACC AAG TGT GTC TAC GTC AAC GAC TGG 1123  
 Pro Lys Lys Cys Ala Lys Gly Thr Lys Cys Val Tyr Val Asn Asp Trp  
                   620                                  625                                  630

TAC TCT CAA TGC CAG CCG AAG AAC TCT TGT GCT TGAGAAGCAA TGCTCACAGC 1176  
 Tyr Ser Gln Cys Gln Pro Lys Asn Ser Cys Ala  
                   635                                  640

ATGTCCTCTT GTCACCCCTT CTTTTCATTC CCAAACATAC TTACTGTATT ATTATTTCCG 1236

ATGCTTCATT TCTTGCTTGT TTCTGTCTTT CCTGCACGCA GCTTTCAACG ATACCCTTCA 1296

TGCGATTGCC CTACGATCAG ATGATGGGCA CGACATGGAG GATGGTTTGG GCACTCACGC 1356

GTTCAGGACG GGAAAATTTA TTAGGGCTGA GATCCGTGAA TTGACTTCAT TTCGGCGGAA 1416

TGTCTGC 1423

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ile Ser Ala Trp Ile Leu Leu Gly Leu Val Gly Ala Val Pro Ser  
   1                  5                                  10                                  15

Ser Val Met Ala Ala Ser Gly Lys Gly His Thr Thr Arg Tyr Trp Asp  
                   20                                  25                                  30

Cys Cys Lys Thr Ser Cys Ala Trp Glu Gly Lys Ala Ser Val Ser Glu  
                   35                                  40                                  45

Pro Val Leu Thr Cys Asn Lys Gln Asp Asn Pro Ile Val Asp Ala Asn  
                   50                                  55                                  60

Ala Arg Ser Gly Cys Asp Gly Gly Gly Ala Phe Ala Cys Thr Asn Asn  
   65                                  70                                  75                                  80

Ser Pro Trp Ala Val Ser Glu Asp Leu Ala Tyr Gly Phe Ala Ala Thr  
                   85                                  90                                  95

Ala Leu Ser Gly Gly Thr Glu Gly Ser Trp Cys Cys Ala Cys Tyr Ala  
                   100                                  105                                  110

Ile Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Val Val Gln  
                   115                                  120                                  125

Ser Thr Asn Thr Gly Gly Asp Leu Ser Asn Asn His Phe Asp Leu Met  
130 135 140

Ile Pro Gly Gly Gly Leu Gly Ile Phe Asp Gly Cys Ser Ala Gln Phe  
145 150 155 160

Gly Gln Leu Leu Pro Gly Glu Arg Tyr Gly Gly Val Ser Ser Arg Ser  
165 170 175

Gln Cys Asp Gly Met Pro Glu Leu Leu Lys Asp Gly Cys Gln Trp Arg  
180 185 190

Phe Asp Trp Phe Lys Asn Ser Asp Asn Pro Asp Ile Glu Phe Glu Gln  
195 200 205

Val Gln Cys Pro Lys Glu Leu Ile Ala Val Ser Gly Cys Val Arg Asp  
210 215 220

Asp Asp Ser Ser Phe Pro Val Phe Gln Gly Ser Gly Ser Gly Asp Val  
225 230 235 240

Asn Pro Pro Pro Lys Pro Thr Thr Thr Thr Thr Ser Ser Lys Pro Lys  
245 250 255

Thr Thr Ser Ala Pro Ser Thr Leu Ser Asn Pro Ser Ala Pro Gln Gln  
260 265 270

Pro Gly Asn Thr Asp Arg Pro Ala Glu Thr Thr Thr Thr Lys Leu Pro  
275 280 285

Ala Leu Pro Ala Thr Thr Ser Ser Pro Ala Val Ser Val Pro Ser Ser  
290 295 300

Ser Ala Arg Val Pro Leu Trp Gly Gln Cys Asp Ser Glu Ala Ser Trp  
305 310 315 320

Asp Ala Pro Lys Lys Cys Ala Lys Gly Thr Lys Cys Val Tyr Val Asn  
325 330 335

Asp Trp Tyr Ser Gln Cys Gln Pro Lys Asn Ser Cys Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 60..956



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCAGCACC CCTCAAGCTG TACAGTTTCC ACCCCGCTCT CTTTCTTCG GCCCCCAGG	59
ATG CGC TCT ACT CCC GTT CTT CGC ACA ACC CTG GCC GCT GCA CTT CCT	107
Met Arg Ser Thr Pro Val Leu Arg Thr Thr Leu Ala Ala Ala Leu Pro	
350 355 360 365	
CTG GTC GCC TCC GCG GCC AGT GGC AGT GGC CAG TCC ACG AGA TAC TGG	155
Leu Val Ala Ser Ala Ala Ser Gly Ser Gly Gln Ser Thr Arg Tyr Trp	
370 375 380	
GAC TGC TGC AAG CCG TCG TGC GCT TGG CCC GGG AAG GCC GCC GTC AGC	203
Asp Cys Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Ala Ala Val Ser	
385 390 395	
CAA CCG GTC TAC GCG TGC GAT GCC AAC TTC CAG CGC CTG TCC GAC TTC	251
Gln Pro Val Tyr Ala Cys Asp Ala Asn Phe Gln Arg Leu Ser Asp Phe	
400 405 410	
AAT GTC CAG TCG GGC TGC AAC GGC GGC TCG GCC TAC TCC TGC GCC GAC	299
Asn Val Gln Ser Gly Cys Asn Gly Gly Ser Ala Tyr Ser Cys Ala Asp	
415 420 425	
CAG ACT CCC TGG GCG GTG AAC GAC AAT CTC GCC TAC GGC TTC GCC GCG	347
Gln Thr Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala	
430 435 440 445	
ACG AGC ATC GCC GGC GGC TCC GAA TCC TCG TGG TGC TGC GCC TGC TAC	395
Thr Ser Ile Ala Gly Gly Ser Glu Ser Ser Trp Cys Cys Ala Cys Tyr	
450 455 460	
GCG CTC ACC TTC ACT TCC GGT CCC GTC GCC GGC AAG ACA ATG GTG GTG	443
Ala Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val	
465 470 475	
CAG TCA ACG AGC ACT GGC GGC GAC CTG GGA AGT AAC CAG TTC GAT ATC	491
Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly Ser Asn Gln Phe Asp Ile	
480 485 490	
GCC ATG CCC GGC GGC GGC GTG GGC ATC TTC AAC GGC TGC AGC TCG CAG	539
Ala Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln	
495 500 505	
TTC GGC GGC CTC CCC GGC GCT CAA TAC GGC GGC ATT TCG TCG CGC GAC	587
Phe Gly Gly Leu Pro Gly Ala Gln Tyr Gly Gly Ile Ser Ser Arg Asp	
510 515 520 525	
CAG TGC GAT TCC TTC CCC GCG CCG CTC AAG CCC GGC TGC CAG TGG CGG	635
Gln Cys Asp Ser Phe Pro Ala Pro Leu Lys Pro Gly Cys Gln Trp Arg	
530 535 540	
TTT GAC TGG TTC CAG AAC GCC GAC AAC CCG ACG TTC ACG TTC CAG CAG	683
Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Thr Phe Thr Phe Gln Gln	
545 550 555	

GTG CAG TGC CCC GCC GAG ATC GTT GCC CGC TCC GGC TGC AAG CGC AAC	731
Val Gln Cys Pro Ala Glu Ile Val Ala Arg Ser Gly Cys Lys Arg Asn	
560 565 570	
GAC GAC TCC AGC TTC CCC GTC TTC ACC CCC CCA AGC GGT GGC AAC GGT	779
Asp Asp Ser Ser Phe Pro Val Phe Thr Pro Pro Ser Gly Gly Asn Gly	
575 580 585	
GGC ACC GGG ACG CCC ACG TCG ACT GCG CCT GGG TCG GGC CAG ACG TCT	827
Gly Thr Gly Thr Pro Thr Ser Thr Ala Pro Gly Ser Gly Gln Thr Ser	
590 595 600 605	
CCC GGC GGC GGC AGT GGC TGC ACG TCT CAG AAG TGG GCT CAG TGC GGT	875
Pro Gly Gly Gly Ser Gly Cys Thr Ser Gln Lys Trp Ala Gln Cys Gly	
610 615 620	
GGC ATC GGC TTC AGC GGA TGC ACC ACC TGT GTC TCT GGC ACC ACC TGC	923
Gly Ile Gly Phe Ser Gly Cys Thr Thr Cys Val Ser Gly Thr Thr Cys	
625 630 635	
CAG AAG TTG AAC GAC TAC TAC TCG CAG TGC CTC TAAACAGCTT TTCGCACGAG	976
Gln Lys Leu Asn Asp Tyr Tyr Ser Gln Cys Leu	
640 645	
GTGGCGGGAC GGAGCAAGGA GACCGTCAAC TTCGTCATGC ATATTTTTTG AGCGCTCAAT	1036
ACATACATAA CCTTCGATTC TTGTACATAG CACGCCGGTA CACATCTCAC ACCGACTTTG	1096
GGGGCGGAAT CAGGCCCGTT TTAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1156
AAAAAAAAAA AAAAAAAAAA	1174

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Arg Ser Thr Pro Val Leu Arg Thr Thr Leu Ala Ala Ala Leu Pro
1 5 10 15
Leu Val Ala Ser Ala Ala Ser Gly Ser Gly Gln Ser Thr Arg Tyr Trp
20 25 30
Asp Cys Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Ala Ala Val Ser
35 40 45
Gln Pro Val Tyr Ala Cys Asp Ala Asn Phe Gln Arg Leu Ser Asp Phe
50 55 60

Asn Val Gln Ser Gly Cys Asn Gly Gly Ser Ala Tyr Ser Cys Ala Asp  
 65 70 75 80  
 Gln Thr Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala  
 85 90 95  
 Thr Ser Ile Ala Gly Gly Ser Glu Ser Ser Trp Cys Cys Ala Cys Tyr  
 100 105 110  
 Ala Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val  
 115 120 125  
 Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly Ser Asn Gln Phe Asp Ile  
 130 135 140  
 Ala Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln  
 145 150 155 160  
 Phe Gly Gly Leu Pro Gly Ala Gln Tyr Gly Gly Ile Ser Ser Arg Asp  
 165 170 175  
 Gln Cys Asp Ser Phe Pro Ala Pro Leu Lys Pro Gly Cys Gln Trp Arg  
 180 185 190  
 Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Thr Phe Thr Phe Gln Gln  
 195 200 205  
 Val Gln Cys Pro Ala Glu Ile Val Ala Arg Ser Gly Cys Lys Arg Asn  
 210 215 220  
 Asp Asp Ser Ser Phe Pro Val Phe Thr Pro Pro Ser Gly Gly Asn Gly  
 225 230 235 240  
 Gly Thr Gly Thr Pro Thr Ser Thr Ala Pro Gly Ser Gly Gln Thr Ser  
 245 250 255  
 Pro Gly Gly Gly Ser Gly Cys Thr Ser Gln Lys Trp Ala Gln Cys Gly  
 260 265 270  
 Gly Ile Gly Phe Ser Gly Cys Thr Thr Cys Val Ser Gly Thr Thr Cys  
 275 280 285  
 Gln Lys Leu Asn Asp Tyr Tyr Ser Gln Cys Leu  
 290 295

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 913 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 41..706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GC	ACT	ATT	TCT	CAG	CTC	CATT	CTC	CCT	TGAA	GTA	ATTC	CACC	ATG	TTC	TCT	CCG	CTC	55
													Met	Phe	Ser	Pro	Leu	
													300					
TGG	GCC	CTG	TCG	GCT	CTG	CTC	CTA	TTT	CCT	GCC	ACT	GAA	GCC	ACT	AGC			103
Trp	Ala	Leu	Ser	Ala	Leu	Leu	Leu	Phe	Pro	Ala	Thr	Glu	Ala	Thr	Ser			
305					310					315					320			
GGC	GTG	ACA	ACC	AGG	TAC	TGG	GAC	TGC	TGC	AAG	CCG	TCT	TGT	GCT	TGG			151
Gly	Val	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Ala	Trp			
				325					330					335				
ACG	GGC	AAA	GCA	TCC	GTC	TCC	AAG	CCC	GTC	GGA	ACC	TGC	GAC	ATC	AAC			199
Thr	Gly	Lys	Ala	Ser	Val	Ser	Lys	Pro	Val	Gly	Thr	Cys	Asp	Ile	Asn			
			340					345						350				
GAC	AAC	GCC	CAG	ACG	CCG	AGC	GAT	CTG	CTC	AAG	TCG	TCC	TGT	GAT	GGC			247
Asp	Asn	Ala	Gln	Thr	Pro	Ser	Asp	Leu	Leu	Lys	Ser	Ser	Cys	Asp	Gly			
		355					360					365						
GGC	AGC	GCC	TAC	TAC	TGC	AGC	AAC	CAG	GGC	CCA	TGG	GCC	GTG	AAC	GAC			295
Gly	Ser	Ala	Tyr	Tyr	Cys	Ser	Asn	Gln	Gly	Pro	Trp	Ala	Val	Asn	Asp			
	370					375					380							
AGC	CTT	TCC	TAC	GGC	TTC	GCT	GCC	GCC	AAG	CTG	TCC	GGA	AAG	CAG	GAG			343
Ser	Leu	Ser	Tyr	Gly	Phe	Ala	Ala	Ala	Lys	Leu	Ser	Gly	Lys	Gln	Glu			
385					390				395						400			
ACT	GAT	TGG	TGC	TGT	GGC	TGC	TAC	AAG	CTC	ACA	TTC	ACC	TCC	ACC	GCC			391
Thr	Asp	Trp	Cys	Cys	Gly	Cys	Tyr	Lys	Leu	Thr	Phe	Thr	Ser	Thr	Ala			
			405					410						415				
GTT	TCC	GGC	AAG	CAA	ATG	ATC	GTG	CAA	ATC	ACG	AAC	ACG	GGC	GGC	GAC			439
Val	Ser	Gly	Lys	Gln	Met	Ile	Val	Gln	Ile	Thr	Asn	Thr	Gly	Gly	Asp			
		420					425						430					
CTC	GGC	AAC	AAC	CAC	TTC	GAC	ATC	GCC	ATG	CCG	GGC	GGC	GGC	GTC	GGC			487
Leu	Gly	Asn	Asn	His	Phe	Asp	Ile	Ala	Met	Pro	Gly	Gly	Gly	Val	Gly			
		435				440					445							
ATC	TTC	AAC	GGG	TGC	TCC	AAG	CAA	TGG	AAC	GGC	ATC	AAT	CTG	GGC	AAC			535
Ile	Phe	Asn	Gly	Cys	Ser	Lys	Gln	Trp	Asn	Gly	Ile	Asn	Leu	Gly	Asn			
	450					455				460								
CAG	TAT	GGC	GGC	TTC	ACT	GAC	CGC	TCG	CAA	TGT	GCG	ACG	CTC	CCG	TCC			583
Gln	Tyr	Gly	Gly	Phe	Thr	Asp	Arg	Ser	Gln	Cys	Ala	Thr	Leu	Pro	Ser			
465					470				475					480				
AAG	TGG	CAG	GCC	AGC	TGC	AAC	TGG	CGC	TTC	GAC	TGG	TTC	GAG	AAT	GCC			631
Lys	Trp	Gln	Ala	Ser	Cys	Asn	Trp	Arg	Phe	Asp	Trp	Phe	Glu	Asn	Ala			
				485				490						495				

GAC AAC CCC ACC GTC GAT TGG GAG CCT GTC ACT TGC CCA CAG GAA TTG 679  
 Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr Cys Pro Gln Glu Leu  
                   500                                  505                                  510

GTC GCC CGG ACT GGC TGT TCC CGT ACC TAAGTGGGGG TGGAACCTCC 726  
 Val Ala Arg Thr Gly Cys Ser Arg Thr  
                   515                                  520

ATGTGAATTG GTGTATATAG CTCCTGCCTG AGCATCCACC AGTTCGCATG TGTGATCAG 786  
 GAGTTGTGTT GCCTTGCTAG GAAAGACTTT GTTGGAACT TCGTGTTTA TTCCAATTGA 846

ATAACCCTGT ATAGACCGGT CACATTTTTC TCTGAAAAA AAAAAAAAAA AAAAAAAAAA 906

AAAAAAA 913

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Phe Ser Pro Leu Trp Ala Leu Ser Ala Leu Leu Leu Phe Pro Ala  
   1                                  5                                  10                                  15

Thr Glu Ala Thr Ser Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys  
                   20                                  25                                  30

Pro Ser Cys Ala Trp Thr Gly Lys Ala Ser Val Ser Lys Pro Val Gly  
                   35                                  40                                  45

Thr Cys Asp Ile Asn Asp Asn Ala Gln Thr Pro Ser Asp Leu Leu Lys  
   50                                  55                                  60

Ser Ser Cys Asp Gly Gly Ser Ala Tyr Tyr Cys Ser Asn Gln Gly Pro  
   65                                  70                                  75                                  80

Trp Ala Val Asn Asp Ser Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu  
                   85                                  90                                  95

Ser Gly Lys Gln Glu Thr Asp Trp Cys Cys Gly Cys Tyr Lys Leu Thr  
                   100                                  105                                  110

Phe Thr Ser Thr Ala Val Ser Gly Lys Gln Met Ile Val Gln Ile Thr  
                   115                                  120                                  125

Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Ile Ala Met Pro  
                   130                                  135                                  140

Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Asn Gly  
   145                                  150                                  155                                  160

Ile Asn Leu Gly Asn Gln Tyr Gly Gly Phe Thr Asp Arg Ser Gln Cys  
165 170 175

Ala Thr Leu Pro Ser Lys Trp Gln Ala Ser Cys Asn Trp Arg Phe Asp  
180 185 190

Trp Phe Glu Asn Ala Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr  
195 200 205

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Cys Pro Gln Glu Leu Val Ala Arg Thr Gly Cys Ser Arg Thr  
210 215 220

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 808 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 37..714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGCTGCTGG GTATATAATG CTCAGACTTG GAACCA ATG GTC CAT CCA AAC ATG	54
Met Val His Pro Asn Met	
225	
CTT AAA ACG CTC GCT CCA TTG ATC ATC TTG GCC GCC TCG GTC ACA GCG	102
Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu Ala Ala Ser Val Thr Ala	
230 235 240	
CAA ACA GCA GGA GTT ACG ACC CGC TAC TGG GAC TGC TGC AAG CCA AGC	150
Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser	
245 250 255 260	
TGT GGA TGG AGT GGA AAG GCT TCT GTT TCT GCT CCA GTC AGA ACT TGC	198
Cys Gly Trp Ser Gly Lys Ala Ser Val Ser Ala Pro Val Arg Thr Cys	
265 270 275	
GAT CGT AAT GGA AAT ACA CTT GGC CCA GAC GTG AAA AGC GGA TGT GAT	246
Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp Val Lys Ser Gly Cys Asp	
280 285 290	
AGC GGT GGA ACG TCA TTC ACT TGC GCG AAC AAT GGT CCA TTT GCG ATT	294
Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn Asn Gly Pro Phe Ala Ile	
295 300 305	
GAC AAT AAC ACT GCA TAT GGT TTT GCT GCA GCC CAC TTA GCG GGC TCT	342
Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala Ala His Leu Ala Gly Ser	
310 315 320	

AGC GAA GCA GCC TGG TGT TGC CAG TGC TAC GAA TTG ACG TTT ACG AGT	390
Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr Glu Leu Thr Phe Thr Ser	
325 330 335 340	
GGA CCC GTA GTT GGG AAG AAA CTG ACC GTT CAA GTC ACA AAC ACG GGA	438
Gly Pro Val Val Gly Lys Lys Leu Thr Val Gln Val Thr Asn Thr Gly	
345 350 355	
GGT GAC CTC GGA AAT AAT CAC TTT GAC CTG ATG ATC CCC GGT GGA GGT	486
Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile Pro Gly Gly Gly	
360 365 370	
GTT GGC CTC TTC ACA CAA GGA TGT CCT GCT CAG TTT GGG AGC TGG AAC	534
Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe Gly Ser Trp Asn	
375 380 385	
GGG GGT GCT CAA TAC GGG GGT GTG TCC AGC CGT GAC CAA TGC TCC CAA	582
Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser Arg Asp Gln Cys Ser Gln	
390 395 400	
CTT CCA GCA GCT GTG CAA GCT GGA TGT CAA TTC CGT TTC GAC TGG ATG	630
Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg Phe Asp Trp Met	
405 410 415 420	
GGT GGC GCG GAT AAC CCC AAC GTC ACC TTC CGA CCT GTG ACC TGC CCA	678
Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro Val Thr Cys Pro	
425 430 435	
GCG CAG CTC ACT AAT ATC TCG GGC TGT GTT CGT AAA TGATTACGA	724
Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys	
440 445	
ATATGTAGTG TCGAATATGT ACATGTGTAT GTACTATAGC TTCAAAGATG GAGGGTCTGT	784
TTAAAAAAAAA AAAAAAAAAA AAAA	808

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val His Pro Asn Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu
1 5 10 15
Ala Ala Ser Val Thr Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp
20 25 30
Asp Cys Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser
35 40 45

Ala Pro Val Arg Thr Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp  
50 55 60

Val Lys Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn  
65 70 75 80

Asn Gly Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala  
85 90 95

Ala His Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr  
100 105 110

Glu Leu Thr Phe Thr Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val  
115 120 125

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu  
130 135 140

Met Ile Pro Gly Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala  
145 150 155 160

Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser  
165 170 175

Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln  
180 185 190

Phe Arg Phe Asp Trp Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe  
195 200 205

Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val  
210 215 220

Arg Lys  
225

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTTGAAC CA ATG GTC CAT CCA AAC ATG CTT AAA ACG CTC GCT CCA  
Met Val His Pro Asn Met Leu Lys Thr Leu Ala Pro  
230 235

48



TTG ATC ATC TTG GCC GCC TCG GTC ACA GCG CAA ACA GCA GGA GTT ACG	96
Leu Ile Ile Leu Ala Ala Ser Val Thr Ala Gln Thr Ala Gly Val Thr	
240 245 250	
ACC CGC TAC TGG GAC TGC TGC AAG CCA AGC TGT GGA TGG AGT GGA AAG	144
Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys	
255 260 265 270	
GCT TCT GTT TCT GCT CCA GTC AGA ACT TGC GAT CGT AAT GGA AAT ACA	192
Ala Ser Val Ser Ala Pro Val Arg Thr Cys Asp Arg Asn Gly Asn Thr	
275 280 285	
CTT GGC CCA GAC GTG AAA AGC GGA TGT GAT AGC GGT GGA ACG TCA TTC	240
Leu Gly Pro Asp Val Lys Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe	
290 295 300	
ACT TGC GCG AAC AAT GGT CCA TTT GCG ATT GAC AAT AAC ACT GCA TAT	288
Thr Cys Ala Asn Asn Gly Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr	
305 310 315	
GGT TTT GCT GCA GCC CAC TTA GCG GGC TCT AGC GAA GCA GCC TGG TGT	336
Gly Phe Ala Ala Ala His Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys	
320 325 330	
TGC CAG TGC TAC GAA TTG ACG TTT ACG AGT GGA CCC GTA GTT GGG AAG	384
Cys Gln Cys Tyr Glu Leu Thr Phe Thr Ser Gly Pro Val Val Gly Lys	
335 340 345 350	
AAA CTG ACC GTT CAA GTC ACA AAC ACG GGA GGT GAC CTC GGA AAT AAT	432
Lys Leu Thr Val Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn	
355 360 365	
CAC TTT GAC CTG ATG ATC CCC GGT GGA GGT GTT GGC CTC TTC ACA CAA	480
His Phe Asp Leu Met Ile Pro Gly Gly Gly Val Gly Leu Phe Thr Gln	
370 375 380	
GGA TGT CCT GCT CAG TTT GGG AGC TGG AAC GGG GGT GCT CAA TAC GGG	528
Gly Cys Pro Ala Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly	
385 390 395	
GGT GTG TCC AGC CGT GAC CAA TGC TCC CAA CTT CCA GCA GCT GTG CAA	576
Gly Val Ser Ser Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln	
400 405 410	
GCT GGA TGT CAA TTC CGT TTC GAC TGG ATG GGT GGC GCG GAT AAC CCC	624
Ala Gly Cys Gln Phe Arg Phe Asp Trp Met Gly Gly Ala Asp Asn Pro	
415 420 425 430	
AAC GTC ACC TTC CGA CCT GTG ACC TGC CCA GCG CAG CTC ACT AAT ATC	672
Asn Val Thr Phe Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile	
435 440 445	
TCG GGC TGT GTT CGT AAA CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC	720
Ser Gly Cys Val Arg Lys Pro Ser Ser Ser Thr Ser Ser Pro Val Asn	
450 455 460	

CAG CCT ACC AGC ACC AGC ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG 768  
 Gln Pro Thr Ser Thr Ser Thr Thr Ser Thr Ser Thr Thr Ser Ser Pro  
 465 470 475

CCA GTC CAG CCT ACG ACT CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT 816  
 Pro Val Gln Pro Thr Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala  
 480 485 490

CAG TGC GGC GGC AAT GGC TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC 864  
 Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly  
 495 500 505 510

AGC ACT TGC ACG AAG ATT AAT GAC TGG TAC CAT CAG TGC CTG 906  
 Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr His Gln Cys Leu  
 515 520

TAGACGCAGG GCAGCTTGAG GGCCTTACTG GTGGCGCAAC GAAATGACAC TCCCAATCAC 966

TGTATTAGTT CTTGTACATA ATTTGTCAT CCCTCCAGGG ATTGTCACAT AAATGCAATG 1026

AGGAACAATG AGTACAGAAT TC 1048

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val His Pro Asn Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu  
 1 5 10 15  
 Ala Ala Ser Val Thr Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp  
 20 25 30  
 Asp Cys Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser  
 35 40 45  
 Ala Pro Val Arg Thr Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp  
 50 55 60  
 Val Lys Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn  
 65 70 75 80  
 Asn Gly Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala  
 85 90 95  
 Ala His Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr  
 100 105 110  
 Glu Leu Thr Phe Thr Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val  
 115 120 125

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu  
 130 135 140  
 Met Ile Pro Gly Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala  
 145 150 155 160  
 Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser  
 165 170 175  
 Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln  
 180 185 190  
 Phe Arg Phe Asp Trp Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe  
 195 200 205  
 Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val  
 210 215 220  
 Arg Lys Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser  
 225 230 235 240  
 Thr Ser Thr Thr Ser Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro  
 245 250 255  
 Thr Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly  
 260 265 270  
 Asn Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr  
 275 280 285  
 Lys Ile Asn Asp Trp Tyr His Gln Cys Leu  
 290 295

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1031 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCATCCAAAC ATG CTT AAA ACG CTC GCT CCA TTG ATC ATC TTG GCC GCC  
 Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu Ala Ala  
 300 305 310

49

TCG GTC ACA GCG CAA ACA GCA GGA GTT ACG ACC CGC TAC TGG GAC TGC	97
Ser Val Thr Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp Asp Cys	
315 320 325	
TGC AAG CCA AGC TGT GGA TGG AGT GGA AAG GCT TCT GTT TCT GCT CCA	145
Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser Ala Pro	
330 335 340	
GTC AGA ACT TGC GAT CGT AAT GGA AAT ACA CTT GGC CCA GAC GTG AAA	193
Val Arg Thr Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp Val Lys	
345 350 355	
AGC GGA TGT GAT AGC GGT GGA ACG TCA TTC ACT TGC GCG AAC AAT GGT	241
Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn Asn Gly	
360 365 370 375	
CCA TTT GCG ATT GAC AAT AAC ACT GCA TAT GGT TTT GCT GCA GCC CAC	289
Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala His	
380 385 390	
TTA GCG GGC TCT AGC GAA GCA GCC TGG TGT TGC CAG TGC TAC GAA TTG	337
Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr Glu Leu	
395 400 405	
ACG TTT ACG AGT GGA CCC GTA GTT GGG AAG AAA CTG ACC GTT CAA GTC	385
Thr Phe Thr Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val Gln Val	
410 415 420	
ACA AAC ACG GGA GGT GAC CTC GGA AAT AAT CAC TTT GAC CTG ATG ATC	433
Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile	
425 430 435	
CCC GGT GGA GGT GTT GGC CTC TTC ACA CAA GGA TGT CCT GCT CAG TTT	481
Pro Gly Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe	
440 445 450 455	
GGG AGC TGG AAC GGG GGT GCT CAA TAC GGG GGT GTG TCC AGC CGT GAC	529
Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser Arg Asp	
460 465 470	
CAA TGC TCC CAA CTT CCA GCA GCT GTG CAA GCT GGA TGT CAA TTC CGT	577
Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg	
475 480 485	
TTC GAC TGG ATG GGT GGC GCG GAT AAC CCC AAC GTC ACC TTC CGA CCT	625
Phe Asp Trp Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro	
490 495 500	
GTG ACC TGC CCA GCG CAG CTC ACT AAT ATC TCG GGC TGT GTT CGT AAA	673
Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys	
505 510 515	
CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC AGC	721
Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser	
520 525 530 535	

ACC	ACG	TCC	ACC	TCC	ACC	ACC	TCG	AGC	CCG	CCA	GTC	CAG	CCT	ACG	ACT	769
Thr	Thr	Ser	Thr	Ser	Thr	Thr	Ser	Ser	Pro	Pro	Val	Gln	Pro	Thr	Thr	
				540					545					550		
CCC	AGC	GGC	TGC	ACT	GCT	GAG	AGG	TGG	GCT	CAG	TGC	GGC	GGC	AAT	GGC	817
Pro	Ser	Gly	Cys	Thr	Ala	Glu	Arg	Trp	Ala	Gln	Cys	Gly	Gly	Asn	Gly	
			555					560					565			
TGG	AGC	GGC	TGC	ACC	ACC	TGC	GTC	GCT	GGC	AGC	ACT	TGC	ACG	AAG	ATT	865
Trp	Ser	Gly	Cys	Thr	Thr	Cys	Val	Ala	Gly	Ser	Thr	Cys	Thr	Lys	Ile	
			570					575					580			
AAT	GAC	TGG	TAC	CAT	CAG	TGC	CTG	TAGACGCAGG	GCAGCTTGAG	GGCCTTACTG						919
Asn	Asp	Trp	Tyr	His	Gln	Cys	Leu									
			585				590									
GTGGCGCAAC	GAAATGACAC	TCCCAATCAC	TGTATTAGTT	CTGTACATA	ATTCGTCAT											979
CCCTCCAGGG	ATTGTCACAT	AAATGCAATG	AGGAACAATG	AGTACAGAAT	TC											1031

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Leu	Lys	Thr	Leu	Ala	Pro	Leu	Ile	Ile	Leu	Ala	Ala	Ser	Val	Thr	
1				5				10						15		
Ala	Gln	Thr	Ala	Gly	Val	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	
			20					25					30			
Ser	Cys	Gly	Trp	Ser	Gly	Lys	Ala	Ser	Val	Ser	Ala	Pro	Val	Arg	Thr	
		35					40					45				
Cys	Asp	Arg	Asn	Gly	Asn	Thr	Leu	Gly	Pro	Asp	Val	Lys	Ser	Gly	Cys	
	50					55					60					
Asp	Ser	Gly	Gly	Thr	Ser	Phe	Thr	Cys	Ala	Asn	Asn	Gly	Pro	Phe	Ala	
65					70					75				80		
Ile	Asp	Asn	Asn	Thr	Ala	Tyr	Gly	Phe	Ala	Ala	Ala	His	Leu	Ala	Gly	
				85					90					95		
Ser	Ser	Glu	Ala	Ala	Trp	Cys	Cys	Gln	Cys	Tyr	Glu	Leu	Thr	Phe	Thr	
			100					105					110			
Ser	Gly	Pro	Val	Val	Gly	Lys	Lys	Leu	Thr	Val	Gln	Val	Thr	Asn	Thr	
			115				120						125			

Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile Pro Gly Gly  
 130 135 140  
 Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe Gly Ser Trp  
 145 150 155 160  
 Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser Arg Asp Gln Cys Ser  
 165 170 175  
 Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg Phe Asp Trp  
 180 185 190  
 Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro Val Thr Cys  
 195 200 205  
 Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys Pro Ser Ser  
 210 215 220  
 Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr Ser  
 225 230 235 240  
 Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly  
 245 250 255  
 Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly  
 260 265 270  
 Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp  
 275 280 285  
 Tyr His Gln Cys Leu  
 290

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 42..971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAACAGTTCA AACACCTACA AGGTCCCGTG CCCTGTAGAC C ATG CGT TCC TCT 53  
 Met Arg Ser Ser  
 295  
 GCA GTC CTC ATC GGC CTC GTG GCC GGT GTG GCC GCC CAG TCC TCT GGC 101  
 Ala Val Leu Ile Gly Leu Val Ala Gly Val Ala Ala Gln Ser Ser Gly  
 300 305 310

ACC	GGC	CGC	ACC	ACC	AGA	TAC	TGG	GAC	TGC	TGC	AAG	CCG	TCC	TGC	GGG	149
Thr	Gly	Arg	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Gly	
	315					320					325					
TGG	GAC	GAA	AAG	GCC	TCC	GTC	AGC	CAG	CCC	GTC	AAG	ACG	TGC	GAT	AGG	197
Trp	Asp	Glu	Lys	Ala	Ser	Val	Ser	Gln	Pro	Val	Lys	Thr	Cys	Asp	Arg	
330					335					340					345	
AAC	AAC	AAC	CCT	CTC	GCG	TCC	ACG	GCC	AGG	AGC	GGC	TGC	GAT	TCC	AAC	245
Asn	Asn	Asn	Pro	Leu	Ala	Ser	Thr	Ala	Arg	Ser	Gly	Cys	Asp	Ser	Asn	
				350					355						360	
GGC	GTC	GCC	TAC	ACG	TGC	AAC	GAT	AAC	CAG	CCG	TGG	GCT	GTC	AAC	GAT	293
Gly	Val	Ala	Tyr	Thr	Cys	Asn	Asp	Asn	Gln	Pro	Trp	Ala	Val	Asn	Asp	
			365					370					375			
AAC	CTG	GCC	TAT	GGT	TTT	GCT	GCC	ACG	GCT	TTC	AGT	GGT	GGA	TCG	GAG	341
Asn	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Thr	Ala	Phe	Ser	Gly	Gly	Ser	Glu	
		380					385					390				
GCC	AGC	TGG	TGC	TGT	GCC	TGC	TAT	GCC	CTT	CAG	TTC	ACC	TCC	GGC	CCT	389
Ala	Ser	Trp	Cys	Cys	Ala	Cys	Tyr	Ala	Leu	Gln	Phe	Thr	Ser	Gly	Pro	
	395					400					405					
GTT	GCG	GGA	AAG	ACC	ATG	GTC	GTC	CAG	TCG	ACA	AAC	ACC	GGC	GGC	GAC	437
Val	Ala	Gly	Lys	Thr	Met	Val	Val	Gln	Ser	Thr	Asn	Thr	Gly	Gly	Asp	
410					415					420					425	
CTC	AGC	GGC	AAC	CAC	TTT	GAC	ATC	CTC	ATG	CCC	GGC	GGC	GGC	CTG	GGC	485
Leu	Ser	Gly	Asn	His	Phe	Asp	Ile	Leu	Met	Pro	Gly	Gly	Gly	Leu	Gly	
				430					435					440		
ATC	TTC	GAC	GGC	TGC	ACC	CCG	CAA	TGG	GGC	GTC	AGC	TTC	CCC	GGA	AAC	533
Ile	Phe	Asp	Gly	Cys	Thr	Pro	Gln	Trp	Gly	Val	Ser	Phe	Pro	Gly	Asn	
			445					450					455			
CGC	TAC	GGC	GGC	ACC	ACC	AGC	CGC	AGC	CAG	TGC	TCC	CAA	ATC	CCC	TCG	581
Arg	Tyr	Gly	Gly	Thr	Thr	Ser	Arg	Ser	Gln	Cys	Ser	Gln	Ile	Pro	Ser	
		460					465					470				
GCC	CTG	CAG	CCC	GGC	TGC	AAC	TGG	CGG	TAC	GAC	TGG	TTC	AAC	GAC	GCC	629
Ala	Leu	Gln	Pro	Gly	Cys	Asn	Trp	Arg	Tyr	Asp	Trp	Phe	Asn	Asp	Ala	
	475					480				485						
GAC	AAC	CCC	GAC	GTC	TCG	TGG	CGC	CGC	GTC	CAG	TGC	CCC	GCC	GCA	CTC	677
Asp	Asn	Pro	Asp	Val	Ser	Trp	Arg	Arg	Val	Gln	Cys	Pro	Ala	Ala	Leu	
	490				495					500					505	
ACC	GAC	CGC	ACC	GGC	TGC	CGC	CGC	TCC	GAT	GAC	GGG	AAC	TAT	CCC	GTC	725
Thr	Asp	Arg	Thr	Gly	Cys	Arg	Arg	Ser	Asp	Asp	Gly	Asn	Tyr	Pro	Val	
				510					515					520		
TTC	CAG	CCC	GGT	CCG	CCC	CCG	GCC	ACG	ACG	ATC	AGG	ACA	TCG	ACT	ACC	773
Phe	Gln	Pro	Gly	Pro	Pro	Pro	Ala	Thr	Thr	Ile	Arg	Thr	Ser	Thr	Thr	
			525					530					535			

C

ATC ACA GCC TCA TCG TCG TCT TCG TCT TCG TCG TCG TCG ACT ACG GCT	821
Ile Thr Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Thr Ala	
540 545 550	
GGT AGC CCG CCT GTG CCG ACT GGT GGT GGT AGT GGG CCA ACG TCG CCT	869
Gly Ser Pro Pro Val Pro Thr Gly Gly Gly Ser Gly Pro Thr Ser Pro	
555 560 565	
GTC TGG GGA CAG TGC GGC GGT CAG GGA TGG AGT GGT CCT ACG CGT TGT	917
Val Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly Pro Thr Arg Cys	
570 575 580 585	
GTT GCT GGG TCG ACA TGC AGT GTG GTC AAC CCG TGG TAC TCG CAG TGT	965
Val Ala Gly Ser Thr Cys Ser Val Val Asn Pro Trp Tyr Ser Gln Cys	
590 595 600	
TTT CCT TAAGGAGCCT CTGGCTGAGC AGATCCTTTC GAAGAGGAGG GTCTCTCTGC	1021
Phe Pro	
TCTTTCAGTC TGTTTCAGGGA ACGGCCGTCT CGGCTACATT GTACATATCC CACCTCGTAT	1081
ATAGCTAGCT CATCTACACT TGTGATCTCC AAAAAAAAAA AAAAAAAAAA A	1132

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Arg Ser Ser Ala Val Leu Ile Gly Leu Val Ala Gly Val Ala Ala	
1 5 10 15	
Gln Ser Ser Gly Thr Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys	
20 25 30	
Pro Ser Cys Gly Trp Asp Glu Lys Ala Ser Val Ser Gln Pro Val Lys	
35 40 45	
Thr Cys Asp Arg Asn Asn Asn Pro Leu Ala Ser Thr Ala Arg Ser Gly	
50 55 60	
Cys Asp Ser Asn Gly Val Ala Tyr Thr Cys Asn Asp Asn Gln Pro Trp	
65 70 75 80	
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Ala Phe Ser	
85 90 95	
Gly Gly Ser Glu Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe	
100 105 110	

C



Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn  
 115 120 125  
 Thr Gly Gly Asp Leu Ser Gly Asn His Phe Asp Ile Leu Met Pro Gly  
 130 135 140  
 Gly Gly Leu Gly Ile Phe Asp Gly Cys Thr Pro Gln Trp Gly Val Ser  
 145 150 155 160  
 Phe Pro Gly Asn Arg Tyr Gly Gly Thr Thr Ser Arg Ser Gln Cys Ser  
 165 170 175  
 Gln Ile Pro Ser Ala Leu Gln Pro Gly Cys Asn Trp Arg Tyr Asp Trp  
 180 185 190  
 Phe Asn Asp Ala Asp Asn Pro Asp Val Ser Trp Arg Arg Val Gln Cys  
 195 200 205  
 Pro Ala Ala Leu Thr Asp Arg Thr Gly Cys Arg Arg Ser Asp Asp Gly  
 210 215 220  
 Asn Tyr Pro Val Phe Gln Pro Gly Pro Pro Pro Ala Thr Thr Ile Arg  
 225 230 235 240  
 Thr Ser Thr Thr Ile Thr Ala Ser Ser Ser Ser Ser Ser Ser Ser  
 245 250 255  
 Ser Thr Thr Ala Gly Ser Pro Pro Val Pro Thr Gly Gly Gly Ser Gly  
 260 265 270  
 Pro Thr Ser Pro Val Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly  
 275 280 285  
 Pro Thr Arg Cys Val Ala Gly Ser Thr Cys Ser Val Val Asn Pro Trp  
 290 295 300  
 Tyr Ser Gln Cys Phe Pro  
 305 310

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 885 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG TTC TCT CCG CTC TGG GCC CTG TCG GCT CTG CTC CTA TTT CCT GCC	48
Met Phe Ser Pro Leu Trp Ala Leu Ser Ala Leu Leu Leu Phe Pro Ala	
315 320 325	
ACT GAA GCC ACT AGC GGC GTG ACA ACC AGG TAC TGG GAC TGC TGC AAG	96
Thr Glu Ala Thr Ser Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys	
330 335 340	
CCG TCT TGT GCT TGG ACG GGC AAA GCA TCC GTC TCC AAG CCC GTC GGA	144
Pro Ser Cys Ala Trp Thr Gly Lys Ala Ser Val Ser Lys Pro Val Gly	
345 350 355	
ACC TGC GAC ATC AAC GAC AAC GCC CAG ACG CCG AGC GAT CTG CTC AAG	192
Thr Cys Asp Ile Asn Asp Asn Ala Gln Thr Pro Ser Asp Leu Leu Lys	
360 365 370	
TCG TCC TGT GAT GGC GGC AGC GCC TAC TAC TGC AGC AAC CAG GGC CCA	240
Ser Ser Cys Asp Gly Gly Ser Ala Tyr Tyr Cys Ser Asn Gln Gly Pro	
375 380 385 390	
TGG GCC GTG AAC GAC AGC CTT TCC TAC GGC TTC GCT GCC GCC AAG CTG	288
Trp Ala Val Asn Asp Ser Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu	
395 400 405	
TCC GGA AAG CAG GAG ACT GAT TGG TGC TGT GGC TGC TAC AAG CTC ACA	336
Ser Gly Lys Gln Glu Thr Asp Trp Cys Cys Gly Cys Tyr Lys Leu Thr	
410 415 420	
TTC ACC TCC ACC GCC GTT TCC GGC AAG CAA ATG ATC GTG CAA ATC ACG	384
Phe Thr Ser Thr Ala Val Ser Gly Lys Gln Met Ile Val Gln Ile Thr	
425 430 435	
AAC ACG GGC GGC GAC CTC GGC AAC AAC CAC TTC GAC ATC GCC ATG CCG	432
Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Ile Ala Met Pro	
440 445 450	
GGC GGC GGC GTC GGC ATC TTC AAC GGC TGC TCC AAG CAA TGG AAC GGC	480
Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Asn Gly	
455 460 465 470	
ATC AAT CTG GGC AAC CAG TAT GGC GGC TTC ACT GAC CGC TCG CAA TGT	528
Ile Asn Leu Gly Asn Gln Tyr Gly Gly Phe Thr Asp Arg Ser Gln Cys	
475 480 485	
GCG ACG CTC CCG TCC AAG TGG CAG GCC AGC TGC AAC TGG CGC TTC GAC	576
Ala Thr Leu Pro Ser Lys Trp Gln Ala Ser Cys Asn Trp Arg Phe Asp	
490 495 500	
TGG TTC GAG AAT GCC GAC AAC CCC ACC GTC GAT TGG GAG CCT GTC ACT	624
Trp Phe Glu Asn Ala Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr	
505 510 515	
TGC CCA CAG GAA TTG GTC GCC CGG ACT GGC TGT TCC CGT ACC CCC TCC	672
Cys Pro Gln Glu Leu Val Ala Arg Thr Gly Cys Ser Arg Thr Pro Ser	
520 525 530	



Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Ile Ala Met Pro  
 130 135 140

Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Asn Gly  
 145 150 155 160

Ile Asn Leu Gly Asn Gln Tyr Gly Gly Phe Thr Asp Arg Ser Gln Cys  
 165 170 175

Ala Thr Leu Pro Ser Lys Trp Gln Ala Ser Cys Asn Trp Arg Phe Asp  
 180 185 190

Trp Phe Glu Asn Ala Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr  
 195 200 205

Cys Pro Gln Glu Leu Val Ala Arg Thr Gly Cys Ser Arg Thr Pro Ser  
 210 215 220

Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr  
 225 230 235 240

Ser Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser  
 245 250 255

Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser  
 260 265 270

Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp  
 275 280 285

Trp Tyr His Gln Cys Leu  
 290

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGATACAA T ATG CGT TCC TCC ACT ATT TTG CAA ACC GGC CTG GTG GCC 50  
 Met Arg Ser Ser Thr Ile Leu Gln Thr Gly Leu Val Ala  
 295 300 305

GTT CTC CCC TTC GCC GTC CAG GCC GCC TCA GGA TCC GGC AAG TCC ACC 98  
 Val Leu Pro Phe Ala Val Gln Ala Ala Ser Gly Ser Gly Lys Ser Thr  
 310 315 320

AGA TAT TGG GAC TGC TGC AAA CCA TCT TGT GCC TGG TCC GGC AAG GCT	146
Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp Ser Gly Lys Ala	
325 330 335	
TCT GTC AAC CGC CCT GTT CTC GCC TGC AAC GCA AAC AAC AAC CCG CTG	194
Ser Val Asn Arg Pro Val Leu Ala Cys Asn Ala Asn Asn Asn Pro Leu	
340 345 350 355	
AAC GAC GCC AAC GTC AAG TCA GGA TGT GAT GGC GGT TCT GCA TAC ACC	242
Asn Asp Ala Asn Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr	
360 365 370	
TGT GCC AAC AAC TCT CCC TGG GCA GTG AAT GAC AAT CTG GCC TAC GGC	290
Cys Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly	
375 380 385	
TTC GCG GCC ACA AAA CTC AGC GGG GGG ACC GAG TCA TCT TGG TGC TGC	338
Phe Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser Trp Cys Cys	
390 395 400	
GCC TGT TAT GCC CTC ACA TTC ACA TCG GGT CCT GTT TCT GGC AAA ACC	386
Ala Cys Tyr Ala Leu Thr Phe Thr Ser Gly Pro Val Ser Gly Lys Thr	
405 410 415	
TTG GTT GTC CAG TCT ACC AGT ACC GGT GGT GAT CTT GGC	425
Leu Val Val Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly	
420 425 430	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Arg Ser Ser Thr Ile Leu Gln Thr Gly Leu Val Ala Val Leu Pro	
1 5 10 15	
Phe Ala Val Gln Ala Ala Ser Gly Ser Gly Lys Ser Thr Arg Tyr Trp	
20 25 30	
Asp Cys Cys Lys Pro Ser Cys Ala Trp Ser Gly Lys Ala Ser Val Asn	
35 40 45	
Arg Pro Val Leu Ala Cys Asn Ala Asn Asn Asn Pro Leu Asn Asp Ala	
50 55 60	
Asn Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Ala Asn	
65 70 75 80	

Asn Ser Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala  
                     85                    90                    95  
 Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser Trp Cys Cys Ala Cys Tyr  
                     100                    105                    110  
 Ala Leu Thr Phe Thr Ser Gly Pro Val Ser Gly Lys Thr Leu Val Val  
                     115                    120                    125  
 Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly  
                     130                    135

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCG GCT TGC GAT AAC GGT GGT GGC ACT GCA TAC ATG TGT GCC AGC CAG	48
Ser Ala Cys Asp Asn Gly Gly Gly Thr Ala Tyr Met Cys Ala Ser Gln	
140                    145                    150	
GAG CCG TGG GCA GTG AGC TCC AAC GTC GCG TAC GGC TTT GCT GCA GTT	96
Glu Pro Trp Ala Val Ser Ser Asn Val Ala Tyr Gly Phe Ala Ala Val	
155                    160                    165                    170	
AGA ATC AGC GGA	108
Arg Ile Ser Gly	

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ala Cys Asp Asn Gly Gly Gly Thr Ala Tyr Met Cys Ala Ser Gln
1                    5                    10                    15

Glu Pro Trp Ala Val Ser Ser Asn Val Ala Tyr Gly Phe Ala Ala Val  
 20 25 30

Arg Ile Ser Gly  
 35

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCC TGC AAC GCA AAC TTC CAG CGC ATC AGT GAC CCC AAC GCC AAG TCG	48
Ala Cys Asn Ala Asn Phe Gln Arg Ile Ser Asp Pro Asn Ala Lys Ser	
40 45 50	
GGC TGC GAT GGT GGC TCG GCC TTC TCT TGC GCC AAA CAA ACC CCT TGG	96
Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Lys Gln Thr Pro Trp	
55 60 65	
GCC	99
Ala	

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Cys Asn Ala Asn Phe Gln Arg Ile Ser Asp Pro Asn Ala Lys Ser
1 5 10 15
Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Lys Gln Thr Pro Trp
20 25 30
Ala

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAC CAG CCG CTC GGC GGA CAA CGG ACG CGA CCA AGG AGC GCG TGC GAC	48
Asp Gln Pro Leu Gly Gly Gln Arg Thr Arg Pro Arg Ser Ala Cys Asp	
35 40 45	
AAT GGC GGC TCT GCA TAC ATG TGC AGC AAC CAG AGC CCG TGG GCC GTC	96
Asn Gly Gly Ser Ala Tyr Met Cys Ser Asn Gln Ser Pro Trp Ala Val	
50 55 60 65	
GAC GAT TCT CTC AGT TAC GGA TGG GCT GCC GTT AGG ATC TAT GGA CAT	144
Asp Asp Ser Leu Ser Tyr Gly Trp Ala Ala Val Arg Ile Tyr Gly His	
70 75 80	
ACC GAA ACT ACT TGG TGC TGC GCT TGC TAC GAG TTG ACT TTT ACC AGC	192
Thr Glu Thr Thr Trp Cys Cys Ala Cys Tyr Glu Leu Thr Phe Thr Ser	
85 90 95	
GGT CCG GTT AGC GGC AAG AAG ATG ATT GTT CAG	225
Gly Pro Val Ser Gly Lys Lys Met Ile Val Gln	
100 105	

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Gln Pro Leu Gly Gly Gln Arg Thr Arg Pro Arg Ser Ala Cys Asp	
1 5 10 15	
Asn Gly Gly Ser Ala Tyr Met Cys Ser Asn Gln Ser Pro Trp Ala Val	
20 25 30	
Asp Asp Ser Leu Ser Tyr Gly Trp Ala Ala Val Arg Ile Tyr Gly His	
35 40 45	



Thr Glu Thr Thr Trp Cys Cys Ala Cys Tyr Glu Leu Thr Phe Thr Ser  
 50 55 60

Gly Pro Val Ser Gly Lys Lys Met Ile Val Gln  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGA AAC GAC AAC CCC ATC TCC AAC ACC AAC GCT GTC AAC GGT TGT GAG	48
Arg Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu	
80 85 90	
GGT GGT GGT TCT GCT TAT GCT TGC ACC AAC TAC TCT CCC TGG GCT GTC	96
Gly Gly Gly Ser Ala Tyr Ala Cys Thr Asn Tyr Ser Pro Trp Ala Val	
95 100 105	
AAC GAT GAG CTT GCC TAC GGT TTC GCT GCT ACC AAG ATC TCC GGT GGC	144
Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Thr Lys Ile Ser Gly Gly	
110 115 120	
TCC GAG GCC AGC TGG TGC TGT GCC TGC TAT CTA	177
Ser Glu Ala Ser Trp Cys Cys Ala Cys Tyr Leu	
125 130	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu	
1 5 10 15	
Gly Gly Gly Ser Ala Tyr Ala Cys Thr Asn Tyr Ser Pro Trp Ala Val	
20 25 30	

Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Thr Lys Ile Ser Gly Gly  
 35 40 45

Ser Glu Ala Ser Trp Cys Cys Ala Cys Tyr Leu  
 50 55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGC GGC TGT GAC GGT GGT TCT GCC TAC GCC TGT GCA AAC AAC TCC CCT	48
Ser Gly Cys Asp Gly Gly Ser Ala Tyr Ala Cys Ala Asn Asn Ser Pro	
60 65 70 75	
TGG GCT GTC AAC GAT	63
Trp Ala Val Asn Asp	
80	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Gly Cys Asp Gly Gly Ser Ala Tyr Ala Cys Ala Asn Asn Ser Pro
1 5 10 15
Trp Ala Val Asn Asp
20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
AAC CAG CCT GTC TTC ACT TGC GAC GCC AAA TTC CAG CGC ATC ACC GAC      48
Asn Gln Pro Val Phe Thr Cys Asp Ala Lys Phe Gln Arg Ile Thr Asp
      25                      30                      35

CCC AAT ACC AAG TCG GGC TGC GAT GGC GGC TCG GCC TTT TCG TGT GCT      96
Pro Asn Thr Lys Ser Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala
      40                      45                      50

GAC CAA ACC CCC TGG GCT CTG AAC GAC GAT TTC GCC TAT GGC TTC GCT      144
Asp Gln Thr Pro Trp Ala Leu Asn Asp Asp Phe Ala Tyr Gly Phe Ala
      55                      60                      65

GCC ACG GCT ATT TCG GGT GGA TCG GAA GCC TCG      177
Ala Thr Ala Ile Ser Gly Gly Ser Glu Ala Ser
      70                      75                      80
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Asn Gln Pro Val Phe Thr Cys Asp Ala Lys Phe Gln Arg Ile Thr Asp
  1              5              10              15

Pro Asn Thr Lys Ser Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala
      20              25              30

Asp Gln Thr Pro Trp Ala Leu Asn Asp Asp Phe Ala Tyr Gly Phe Ala
      35              40              45

Ala Thr Ala Ile Ser Gly Gly Ser Glu Ala Ser
      50              55
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
GTC TAC GCC TGC AAC GCA AAC TTC CAG CGC ATC ACC GAC GCC AAC GCC      48
Val Tyr Ala Cys Asn Ala Asn Phe Gln Arg Ile Thr Asp Ala Asn Ala
  60                      65                      70                      75

AAG TCC GGC TGC GAT GGC GGC TCC GCC TTC TCG TGC GCC AAC CAG ACC      96
Lys Ser Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Asn Gln Thr
                      80                      85                      90

CCG TGG GCC GTG AGC GAC GAC TTT GCC TAC GGT TTC GCG GCT ACG GCG     144
Pro Trp Ala Val Ser Asp Asp Phe Ala Tyr Gly Phe Ala Ala Thr Ala
                      95                      100                      105

CTC GCC GGC                                                                153
Leu Ala Gly
  110
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Val Tyr Ala Cys Asn Ala Asn Phe Gln Arg Ile Thr Asp Ala Asn Ala
  1                      5                      10                      15

Lys Ser Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Asn Gln Thr
                20                      25                      30

Pro Trp Ala Val Ser Asp Asp Phe Ala Tyr Gly Phe Ala Ala Thr Ala
  35                      40                      45

Leu Ala Gly
  50
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTC AAC CGC CCT GTC CTC GCC TGC GAC GCA AAC AAC AAC CCT CTG ACC	48
Val Asn Arg Pro Val Leu Ala Cys Asp Ala Asn Asn Asn Pro Leu Thr	
55 60 65	
GAC GCC GGC GTC AAG TCC GGA TGT GAT GGC GGT TCT GCA TAC ACC TGT	96
Asp Ala Gly Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys	
70 75 80	
GCC AAC AAC TCC CCA TGG GCA GTG AAC GAC CAG CTC GCC TAC GGC TTT	144
Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe	
85 90 95	
GCC GCC ACC AAA CTG AGC GGC GGA ACT GAG TCG TCA	180
Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Asn Arg Pro Val Leu Ala Cys Asp Ala Asn Asn Asn Pro Leu Thr	
1 5 10 15	
Asp Ala Gly Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys	
20 25 30	
Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe	
35 40 45	
Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser	
50 55 60	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
GGC TGC GAC GGC GGC AGC GCC TTC ACC TGC TCC AAC AAC TCT CCA TGG 48
Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser Pro Trp
      65              70              75

GCT GTG AAC GAA GAT 63
Ala Val Asn Glu Asp
      80
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser Pro Trp
  1              5              10              15
Ala Val Asn Glu Asp
      20
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
ACA AGA AAC GAC GGC CCC CTG TCC AGC CCC GAT GCC GCC TCC GGC TGT 48
Thr Arg Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser Gly Cys
      25              30              35
```

GAT	GGC	GGC	GAA	GCC	TTT	GCC	TGT	TCT	AAT	ACC	TCG	CCT	TGG	GCC	GTC	96
Asp	Gly	Gly	Glu	Ala	Phe	Ala	Cys	Ser	Asn	Thr	Ser	Pro	Trp	Ala	Val	
		40					45					50				

ACC GAG TCA  
Thr Glu Ser  
70

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

Thr Arg Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser Gly Cys  
1 5 10 15

Thr Glu Ser  
50

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

140

C

CCA AGT GGG TGT GAC GGT GGT AGC GCC TTC ACT TGT TCC AAC AAC TCC 96  
 Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser  
           70                          75                          80

CCG TGG GCA GTC GAT GAC CAG ACA GCT TAT GGC TTT GCG GCA ACA GCC 144  
 Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe Ala Ala Thr Ala  
           85                          90                          95

ATC AGT GGC CAG TCC 159  
 Ile Ser Gly Gln Ser  
 100

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Val Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser Asp Pro Asn Ala  
   1                  5                          10                          15  
 Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser  
                   20                          25                          30  
 Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe Ala Ala Thr Ala  
           35                          40                          45  
 Ile Ser Gly Gln Ser  
       50

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGT GAG AAG AAC GAC AAC CCC TTA GCT GAC TTC AGC ACG AAA TCC GGG 48  
 Cys Glu Lys Asn Asp Asn Pro Leu Ala Asp Phe Ser Thr Lys Ser Gly  
       55                          60                          65



TGT GAA AGC GGA GGT TCG GCT TAT ACG TGT AAC AAC CAA TCA CCA TGG 96  
 Cys Glu Ser Gly Gly Ser Ala Tyr Thr Cys Asn Asn Gln Ser Pro Trp  
 70 75 80 85

GCC GTC AAT GAC TTG GTG TCG TAT GGC TTC GCC GCC ACA GCG ATC AAT 144  
 Ala Val Asn Asp Leu Val Ser Tyr Gly Phe Ala Ala Thr Ala Ile Asn  
 90 95 100

GGT GGC AAT 153  
 Gly Gly Asn

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Cys Glu Lys Asn Asp Asn Pro Leu Ala Asp Phe Ser Thr Lys Ser Gly  
 1 5 10 15

Cys Glu Ser Gly Gly Ser Ala Tyr Thr Cys Asn Asn Gln Ser Pro Trp  
 20 25 30

Ala Val Asn Asp Leu Val Ser Tyr Gly Phe Ala Ala Thr Ala Ile Asn  
 35 40 45

Gly Gly Asn  
 50

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGC CGC CCC GTC GGA ACC TGC AAG AGG AAC GAC AAC CCC CTC TCC GAC 48  
 Ser Arg Pro Val Gly Thr Cys Lys Arg Asn Asp Asn Pro Leu Ser Asp  
 55 60 65

CCC GAT GCC AAG TCC GGC TGC GAC GGC GGC GGC GCC TTC ATG TGC TCC 96  
 Pro Asp Ala Lys Ser Gly Cys Asp Gly Gly Gly Ala Phe Met Cys Ser  
           70                      75                      80

ACC CAG CAG CCG TGG GCC GTC AAC GAC AAT CTG GCA TAT GGC TTC GCC 144  
 Thr Gln Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala  
           85                      90                      95

GCC ACG GCC ATC AGC GGC GGC AAC GAG 171  
 Ala Thr Ala Ile Ser Gly Gly Asn Glu  
 100                      105

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Pro Val Gly Thr Cys Lys Arg Asn Asp Asn Pro Leu Ser Asp  
   1                      5                      10                      15

Pro Asp Ala Lys Ser Gly Cys Asp Gly Gly Gly Ala Phe Met Cys Ser  
           20                      25                      30

Thr Gln Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala  
           35                      40                      45

Ala Thr Ala Ile Ser Gly Gly Asn Glu  
   50                      55

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACT TGC AAC AAG AAC GAC GGG CCC CTG TCC AGC CCC GAT GCC GCC TCC 48  
 Thr Cys Asn Lys Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser  
           60                      65                      70

GGC TGT GAT GGC GGC GAA GCC TTT GCC TGT TCT AAT ACC TCG CCT TGG 96  
 Gly Cys Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp  
       75                      80                      85

GCC GTC AGC GAC CAG CTC GCG TAC GGA TAC CTC GCC ACG TCC ATC TCC 144  
 Ala Val Ser Asp Gln Leu Ala Tyr Gly Tyr Leu Ala Thr Ser Ile Ser  
       90                      95                      100                      105

GGC GGC ACC GAG TCG 159  
 Gly Gly Thr Glu Ser  
                       110

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Thr Cys Asn Lys Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser  
   1                      5                      10                      15

Gly Cys Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp  
           20                      25                      30

Ala Val Ser Asp Gln Leu Ala Tyr Gly Tyr Leu Ala Thr Ser Ile Ser  
       35                      40                      45

Gly Gly Thr Glu Ser  
       50

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCA GTT TTC TCC TGT GAC AAG TAC GAC AAC CCT CTA CCT GAC GCC AAT 48  
 Pro Val Phe Ser Cys Asp Lys Tyr Asp Asn Pro Leu Pro Asp Ala Asn  
       55                      60                      65

134

C

GCT GTG TCC GGG TGT GAC CCC GGA GGT ACT GCC TTC  
 Ala Val Ser Gly Cys Asp Pro Gly Gly Thr Ala Phe  
 70 75 80

84

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Val Phe Ser Cys Asp Lys Tyr Asp Asn Pro Leu Pro Asp Ala Asn  
 1 5 10 15  
 Ala Val Ser Gly Cys Asp Pro Gly Gly Thr Ala Phe  
 20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACC TGC GAC GCC TGC GAC AGC CCC CTC AGC GAC TAC GAC GCC AAG TCC 48  
 Thr Cys Asp Ala Cys Asp Ser Pro Leu Ser Asp Tyr Asp Ala Lys Ser  
 30 35 40  
 GGC TGC GAC GGC GGT AGC GCA TAC ACC TGC ACC TAC TCT ACC CCC TGG 96  
 Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Thr Tyr Ser Thr Pro Trp  
 45 50 55 60  
 GCC GTC GAC GAC AAC CTC TCC TAC GGT TTC GCC GCC GCC AAG CTG AGC 144  
 Ala Val Asp Asp Asn Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu Ser  
 65 70 75  
 GGA 147  
 Gly

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr Cys Asp Ala Cys Asp Ser Pro Leu Ser Asp Tyr Asp Ala Lys Ser  
1 5 10 15  
Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Thr Tyr Ser Thr Pro Trp  
20 25 30  
Ala Val Asp Asp Asn Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu Ser  
35 40 45  
Gly

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCA CTA GCA GAT TTC ACC GGT GGA ACC GGC TGT AAT GGC GGT TCG ACA 48  
Pro Leu Ala Asp Phe Thr Gly Gly Thr Gly Cys Asn Gly Gly Ser Thr  
50 55 60 65  
TTC TCA TGC TCA AAC CAA CAA CCA TGG GCG GTC AAC GAC ACA TTC TCG 96  
Phe Ser Cys Ser Asn Gln Gln Pro Trp Ala Val Asn Asp Thr Phe Ser  
70 75 80  
TAC GGC TTT GCG GGC ATC TTT ATC ACA GGC CAT GTC GAG 135  
Tyr Gly Phe Ala Gly Ile Phe Ile Thr Gly His Val Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Pro Leu Ala Asp Phe Thr Gly Gly Thr Gly Cys Asn Gly Gly Ser Thr
 1             5             10             15
Phe Ser Cys Ser Asn Gln Gln Pro Trp Ala Val Asn Asp Thr Phe Ser
      20             25             30
Tyr Gly Phe Ala Gly Ile Phe Ile Thr Gly His Val Glu
 35             40             45
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
GCC AAA TCT GGA TGT GAT GCT GGT GGA GGT CAA GCC TAC ATG TGC TCC      48
Ala Lys Ser Gly Cys Asp Ala Gly Gly Gly Gln Ala Tyr Met Cys Ser
      50             55             60
AAC CAA CAA CCT TGG GTA GTC AAC GAC AAC CTC GCC TAC GGT TTC GCC      96
Asn Gln Gln Pro Trp Val Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala
      65             70             75
GCA GTC AAC ATT GCC GGC      114
Ala Val Asn Ile Ala Gly
      80
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ala Lys Ser Gly Cys Asp Ala Gly Gly Gly Gln Ala Tyr Met Cys Ser  
 1 5 10 15  
 Asn Gln Gln Pro Trp Val Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala  
 20 25 30  
 Ala Val Asn Ile Ala Gly  
 35

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

T TCG ACG TCC GGG TGC GAC AAT GGC GGC AGC GCC TTC ATG TGC TCT 46  
 Ser Thr Ser Gly Cys Asp Asn Gly Gly Ser Ala Phe Met Cys Ser  
 40 45 50  
 AAC CAA AGC CCC TGG GCC GTC AAC GAC GAT CTG GCC TAC GGC TGG GCC 94  
 Asn Gln Ser Pro Trp Ala Val Asn Asp Asp Leu Ala Tyr Gly Trp Ala  
 55 60 65  
 GCC GTC TCA ATC GCG GGC C 113  
 Ala Val Ser Ile Ala Gly  
 70 75

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Thr Ser Gly Cys Asp Asn Gly Gly Ser Ala Phe Met Cys Ser Asn  
 1 5 10 15  
 Gln Ser Pro Trp Ala Val Asn Asp Asp Leu Ala Tyr Gly Trp Ala Ala  
 20 25 30

Val Ser Ile Ala Gly  
35

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCA ACA CCG GTG CAG ACG TGC GAC CGC AAC GAC AAC CCG CTC TAC GAC	48
Ser Thr Pro Val Gln Thr Cys Asp Arg Asn Asp Asn Pro Leu Tyr Asp	
40 45 50	
GGC GGG TCG ACG CGG TCC GGC TGC GAC GCC GGC GGC GGC GCC TAC ATG	96
Gly Gly Ser Thr Arg Ser Gly Cys Asp Ala Gly Gly Gly Ala Tyr Met	
55 60 65	
TGC TCG TCG CAC AGC CCG TGG GCC GTC AGC GAC AGC CTC TCG TAC GGC	144
Cys Ser Ser His Ser Pro Trp Ala Val Ser Asp Ser Leu Ser Tyr Gly	
70 75 80 85	
TGG GCG GCC GTC CGC ATC GCC GGC CAG TCC GAG	177
Trp Ala Ala Val Arg Ile Ala Gly Gln Ser Glu	
90 95	

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Thr Pro Val Gln Thr Cys Asp Arg Asn Asp Asn Pro Leu Tyr Asp	
1 5 10 15	
Gly Gly Ser Thr Arg Ser Gly Cys Asp Ala Gly Gly Gly Ala Tyr Met	
20 25 30	
Cys Ser Ser His Ser Pro Trp Ala Val Ser Asp Ser Leu Ser Tyr Gly	
35 40 45	



Trp Ala Ala Val Arg Ile Ala Gly Gln Ser Glu  
 50 55

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AAC GAC AAC CCC ATC TCC AAC ACC AAC GCT GTC AAC GGT TGT GAG GGT	48
Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu Gly	
60 65 70 75	
GGT GGT TCT GCT TAC GCT TGC TCC AAC TAC TCT CCC TGG GCT GTC AAC	96
Gly Gly Ser Ala Tyr Ala Cys Ser Asn Tyr Ser Pro Trp Ala Val Asn	
80 85 90	
GAT GAC CTT GCC TAC GGT TTC GCT GTT ACC AAG ATC TCC GGT GGC TCC	144
Asp Asp Leu Ala Tyr Gly Phe Ala Val Thr Lys Ile Ser Gly Gly Ser	
95 100 105	
GAG GCC	150
Glu Ala	

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu Gly	
1 5 10 15	
Gly Gly Ser Ala Tyr Ala Cys Ser Asn Tyr Ser Pro Trp Ala Val Asn	
20 25 30	
Asp Asp Leu Ala Tyr Gly Phe Ala Val Thr Lys Ile Ser Gly Gly Ser	
35 40 45	

Glu Ala  
50

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTC AAT CAG CCC ATC CGA ACG TGT AGT GCC AAC GAC TCG CCC TTG TCC	48
Val Asn Gln Pro Ile Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser	
55 60 65	
GAC CCA AAT ACC CCA AGT GGC TGT GAC GGT GGT AGC GCC TTC ACT TGT	96
Asp Pro Asn Thr Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys	
70 75 80	
TCC AAC AAC TCC CCG TGG GCA GTC GAT GAC CAG ACA GCT TAT GGC TTT	144
Ser Asn Asn Ser Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe	
85 90 95	
GCG GCA ACA GCC ATC AGT GGC CAG TCC GAG AGC AGC	180
Ala Ala Thr Ala Ile Ser Gly Gln Ser Glu Ser Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Asn Gln Pro Ile Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser	
1 5 10 15	
Asp Pro Asn Thr Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys	
20 25 30	
Ser Asn Asn Ser Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe	
35 40 45	

Ala Ala Thr Ala Ile Ser Gly Gln Ser Glu Ser Ser  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACC TGC GAC AAG AAG GAC AAC CCC ATC TCT GAT GCC AAC GCC AAG AGC	48
Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asp Ala Asn Ala Lys Ser	
65 70 75	
GGC TGT GAT GGC GGT TCT GCT TTC GCC TGC ACC AAC TAC TCT CCC TTC	96
Gly Cys Asp Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro Phe	
80 85 90	
GCC GTC AAC GAC AAC CTC GCC TAC GGT TTC GCT GCC ACC AAG CTT GCT	144
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu Ala	
95 100 105	
GGA GGC TCC GAG GCT	159
Gly Gly Ser Glu Ala	
110	

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asp Ala Asn Ala Lys Ser	
1 5 10 15	
Gly Cys Asp Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro Phe	
20 25 30	
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu Ala	
35 40 45	

Gly Gly Ser Glu Ala  
50

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACC TGC TAC GCC AAT GAC CAG CGC ATC GCC GAC CGC AGC ACC AAG TCC	48
Thr Cys Tyr Ala Asn Asp Gln Arg Ile Ala Asp Arg Ser Thr Lys Ser	
55 60 65	
GGC TGC GAC GGC GGC TCG GCC TAC TCC TGT TCT	81
Gly Cys Asp Gly Gly Ser Ala Tyr Ser Cys Ser	
70 75 80	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Cys Tyr Ala Asn Asp Gln Arg Ile Ala Asp Arg Ser Thr Lys Ser	
1 5 10 15	
Gly Cys Asp Gly Gly Ser Ala Tyr Ser Cys Ser	
20 25	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
ACC TGT GAC AAG AAG GAC AAC CCC ATC TCA AAC TTG AAC GCT GTC AAC      48
Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asn Leu Asn Ala Val Asn
      30              35              40
GGT TGT GAG GGT GGT GGT TCT GCC TTC GCC TGC ACC AAC TAC TCT CCT      96
Gly Cys Glu Gly Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro
      45              50              55
TGG GCG GTC AAT GAC AAC CTT GCC TAC GGC TTC GCT GCA ACC AAG CTT      144
Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu
      60              65              70              75
GCC GGT GGC TCC GAG G
Ala Gly Gly Ser Glu
      80
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asn Leu Asn Ala Val Asn
  1              5              10              15
Gly Cys Glu Gly Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro
      20              25              30
Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu
      35              40              45
Ala Gly Gly Ser Glu
      50
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CCA	GTA	GGC	ACC	TGC	GAC	GCC	GGC	AAC	AGC	CCC	CTC	GGC	GAC	CCC	CTG	48	
Pro	Val	Gly	Thr	Cys	Asp	Ala	Gly	Asn	Ser	Pro	Leu	Gly	Asp	Pro	Leu		
				55					60					65			
GCC	AAG	TCT	GGC	TGC	GAG	GGC	GGC	CCG	TCG	TAC	ACG	TGC	GCC	AAC	TAC	96	
Ala	Lys	Ser	Gly	Cys	Glu	Gly	Gly	Pro	Ser	Tyr	Thr	Cys	Ala	Asn	Tyr		
70					75					80					85		
CAG	CCG	TGG	GCG	GTC	AAC	GAC	CAG	CTG	GCC	TAC	GGC	TTC	GCG	GCC	ACG	144	
Gln	Pro	Trp	Ala	Val	Asn	Asp	Gln	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Thr		
				90					95					100			
GCC	ATC	AAC	GGC	GGC	ACC	GAG										165	
Ala	Ile	Asn	Gly	Gly	Thr	Glu											
				105													

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro	Val	Gly	Thr	Cys	Asp	Ala	Gly	Asn	Ser	Pro	Leu	Gly	Asp	Pro	Leu	
1					5					10					15	
Ala	Lys	Ser	Gly	Cys	Glu	Gly	Gly	Pro	Ser	Tyr	Thr	Cys	Ala	Asn	Tyr	
				20					25					30		
Gln	Pro	Trp	Ala	Val	Asn	Asp	Gln	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Thr	
				35					40					45		
Ala	Ile	Asn	Gly	Gly	Thr	Glu										
				50												55

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Trp Cys Cys Xaa Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Trp Cys Cys Xaa Cys Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Xaa Pro Gly Gly Gly Xaa Gly Xaa Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

---

Gly	Cys	Xaa	Xaa	Arg	Xaa	Asp	Trp	Xaa
1				5				

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCCAAGCTT ACNMGNTAYT GGGAYTGYTG YAARMC

36

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTAGTCTAGA TARCANGCRC ARCACC

26

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTAGTCTAGA AANADNCCNA VNCCNCCNCC NGG

33



(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAGTCTAGA NAACCARTCA RWANCKCC

28

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGGAGCTCAC GTCCAAGAGC GGCTGCTCCC GTCCCTCCAG CAGCACCAGC TCTCCGG

57

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CCGGAGAGCT GGTGCTGCTG GAGGGACGGG AGCAGCCGCT CTTGGACGTG AGCTCCG

57

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CGGAGCTCAC GTCCAAGAGC GGCTGCTCCC GTAACGACGA CGGCAACTTC CCTGCCG

57

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CGGCAGGGAA GTTGCCGTCG TCGTTACGGG AGCAGCCGCT CTTGGACGTG AGCTCCG

57

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAACATCACA TCAAGCTCTC C

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCCCATCCTT TAACTATAGC G

21

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGTCGCCCCGG ACTGGCTGTT CCCGTACCCC CTCCAGCAGC ACCAGCTCTC CGG

53

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CCGGAGAGCT GGTGCTGCTG GAGGGGGTAC GGGAACAGCC AGTCCGGGCG ACC

53

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGGACTACTA GCAGCTGTAA TACG

24

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GACCGGAGAG CTGGTGCTGC TGGAGGGTTT ACGAACACAG CCCGAGATAT TAGTG

55

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CCCCAAGCTT GACTTGGAAC CAATGGTCCA TCC

33

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(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCCCAAGCTT CCATCCAAAC ATGCTTAAAA CGCTCG

36

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CACTAATATC TCGGGCTGTG TTCGTAAACC CTCCAGCAGC ACCAGCTCTC CGGTC

55

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGCGTGAAT GTAAGCGTGA CATA

24

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Ala	Trp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Thr	Ser	Cys	Ala	Trp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Gly	Trp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Xaa	Thr	Arg	Xaa	Phe	Asp	Xaa
1				5		

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Xaa Thr Arg Xaa Tyr Asp Xaa  
 1 5

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Xaa Thr Arg Xaa Trp Asp Xaa  
 1 5

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Trp Cys Cys Xaa Cys  
1 5

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